



<110> Renauld, Jean-Christophe
Dumoutier, Laure

<120> Isolated Nucleic Acid Molecules Which Encode A Soluble IL-TIF/IL-22
Receptor or Binding Protein Which Binds to IL-TIF/IL-22, And Uses Thereof

<130> LUD 5684.2 (10106926)

<140> US 09/919,162

<141> 2001-31-07

<150> US 60/245,495

<151> 2000-03-11

<150> US 60/234,583

<151> 2000-09-22

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<212> DNA

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actggcaaca	gcagtgtcta	ttttgtgcag	tacaaaatat	atggacagag	acaatggaaa	240
aataaagaag	actgttgggg	tactcaagaa	ctctcttgtg	accttaccag	tgaaacctca	300
gacatacagg	aaccttatta	cgggaggggtg	agggcggcct	cggctgggag	ctactcagaa	360
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aataaacc	aagtcaatgg	ctctttgttg	gtaattctcc	atgctccaaa	tttaccatat	480
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tttataatta	acaattcact	agaaaaggag	caaaagggtt	atgaaggggc	tcacagagcg	600
gttgaaattg	aagctctaac	accacactcc	agctactgtg	tagtggctga	aatatatcag	660
cccatgttag	acagaagaag	tcagagaagt	gaagagagat	gtgtggaaat	tccatgactt	720
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			20					25					30		
Val	Gln	Phe	Gln	Ser	Arg	Asn	Phe	His	Asn	Ile	Leu	Gln	Trp	Gln	Pro
		35					40					45			
Gly	Arg	Ala	Leu	Thr	Gly	Asn	Ser	Ser	Val	Tyr	Phe	Val	Gln	Tyr	Lys
	50					55					60				
Ile	Tyr	Gly	Gln	Arg	Gln	Trp	Lys	Asn	Lys	Glu	Asp	Cys	Trp	Gly	Thr
65				70						75				80	
Gln	Glu	Leu	Ser	Cys	Asp	Leu	Thr	Ser	Glu	Thr	Ser	Asp	Ile	Gln	Glu
			85					90					95		
Pro	Tyr	Tyr	Gly	Arg	Val	Arg	Ala	Ala	Ser	Ala	Gly	Ser	Tyr	Ser	Glu
			100				105						110		
Trp	Ser	Met	Thr	Pro	Arg	Phe	Thr	Pro	Trp	Trp	Glu	Thr	Lys	Ile	Asp
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Leu	His	Ala	Pro	Asn	Leu	Pro	Tyr	Arg	Tyr	Gln	Lys	Glu	Lys	Asn	Val
145				150						155				160	
Ser	Ile	Glu	Asp	Tyr	Tyr	Glu	Leu	Leu	Tyr	Arg	Val	Phe	Ile	Ile	Asn
			165						170				175		
Asn	Ser	Leu	Glu	Lys	Glu	Gln	Lys	Val	Tyr	Glu	Gly	Ala	His	Arg	Ala
		180					185					190			
Val	Glu	Ile	Glu	Ala	Leu	Thr	Pro	His	Ser	Ser	Tyr	Cys	Val	Val	Ala
	195					200					205				
Glu	Ile	Tyr	Gln	Pro	Met	Leu	Asp	Arg	Arg	Ser	Gln	Arg	Ser	Glu	Glu
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 tttcacaaca ttttgcaatg gcagcctggg agggcactta ctggcaacag cagtgtctat 180
 tttgtgcagt acaaaatcat gttctcatgc agcatgaaaa gctctcacca gaagccaagt 240
 ggatgctggc agcacatttc ttgtaacttc ccaggctgca gaacattggc taaatatgga 300
 cagagacaat ggaaaaataa agaagactgt tggggacttc aagaactctc ttgtgacctt 360
 accagtgaac cctcagacat acaggaacct tattacggga ggggtgagggc ggcctcggct 420
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 gatcctccag tcatgaatat aaccaagtc aatggctctt tgttggtaat tctccatgct 540
 ccaaattttac catatagata ccaaaggaa aaaaatgtat ctatagaaga ttactatgaa 600
 ctactatacc gagtttttat aattaacaat tctactagaa aggagcaaaa ggtttatgaa 660
 ggggctcaca gagcgggttg aattgaagct ctaacaccac actccagcta ctgtgtagtg 720
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 Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln
 35 40 45
 Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr
 50 55 60
 Lys Ile Met Phe Ser Cys Ser Met Lys Ser Ser His Gln Lys Pro Ser
 65 70 75 80
 Gly Cys Trp Gln His Ile Ser Cys Asn Phe Pro Gly Cys Arg Thr Leu
 85 90 95
 Ala Lys Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly

-4-